_						
54 GAG	108 GCC A	162 CTG L	216 AT'C I	270 AGG R	324 CCC P	378 ATC I
299	GCT	999	TGC	GAC	ACC T	GCC
AGT	ATG M	9	CTC	299	TTC	ATG M
45 GAA	99 ATC	153 AGC S	207 GGC G	261 AGC S	315 GAC D	369 CTC L
GGA	GAG	GAG E	CTT L	GCC	CGC R	ATA I
GGA	CCA	${ m CTG}$	CTG L	GCG A	CGG R	CGC R
36 GAG	90 ACT	144 GAT D	198 CTG L	252 CCG P	306 AAG K	360 CCG P
	TTT	AGC	${ m CTG}$	CAG Q	CTC L	GAC D
CGC TCA	ACC	CCA	AAC N	GAC D	CGC	CAG Q
27 GCT	81 CCA	135 GAC D	189 CTC L	243 GGG G	297 CCC P	351 GTC V
CI'C	299	GCC	CCG P	CGC R	${ m CTG}$	9 299
CCA	ວອວ	9 299	TCG	GTG V	CCT	GAC D
18 GCG	72 TAG	126 ACT T	180 ACG T	234 ATC I	288 CCC P	342 TTC F
292	၁၁၅	GCG A	TTC	AAG K	CCG P	CGC R
೨೨೨	CCT GCC	GTG V	ATT I	TAC Y	ANG	CGG R
9 GAA	63 ATC	117 GTG V	171 GAG E	225 CTC L	279 ACG T	333 CTG L
GCC GCC GAA CCC CGC	990	GAT D	CAT H	${ m CTG}$	ACG	GCC GAG (
၁၁၅	63 TTC CGG ATC	GAG	CTG L	TTC	ACG 7	GCC A
-						

FIG. 1A

432	486	540	594	618	702	756
GGG	TGC	GCT	CAT '	GAG	AGT	AAA
G	C	A	H	E	S	K
GAG E	TTT	ACT T	TAT Y	GAT D	GGA G	TTT
CCC	ACA T	CTC	AAG K	TCA	AGT S	GTC V
423	477	531	585	639	693	747
GGG	GCC	GAC	TTC	TAC	TTC	TNT
G	A	D	F	Y	F	X
T'AC Y	$\mathrm{CT'}\Gamma$	TCT S	ACT T	GTG V		CAC
TTC	9 299	CTT	T'TC F	ACT T	AAA K	GTC V
414	468	522	576	630		738
AAA	AGG	GAC	CAG	CCC		ACA
K	R	D	Q	P		T'
CGC	TCC	GAT	TCT	GAG	AAT	GTA
R	S	D	S		N	V
9	GCA	TAC	GAG	GAG	AAA	TTT
299	A	Y	E	E	K	
405	459	513	567	621	675	729
AAA	GAT	GAG	TGG	GGG	CGG	TCA
K	D	E	W	G	R	S
ACC	AGA	GAT	GAC	GAG	TCC	AAA
T	R	D	D	E		K
GTG	GGN	AAG	AGT	AAG	AGT	GCA
V	G	K	S	K		A
396	450	504	558	612	666	720
GAT'	GCT	CTG	CTG	CTG	GAG	TTT
D	A	L	L	L	E	F
TTC	TTT	GCA A	ACT	CTG L	GAT D	TAT Y
GTG V	GTC V	GAA	GAG	AAA K	AAA K	N'TG X
387	441	495	549	603	657	711
AAG	GGG	AAG	CAG	GGC	CCA	ATN
K	G	K	Q	G	P	X
		GAT D	CAG Q	GTG V		TCT S
AAC	d	C'I'G	OCC	CAC	GAA	ATA
N	SCC	L	V	H	E	I

FIG. 1B

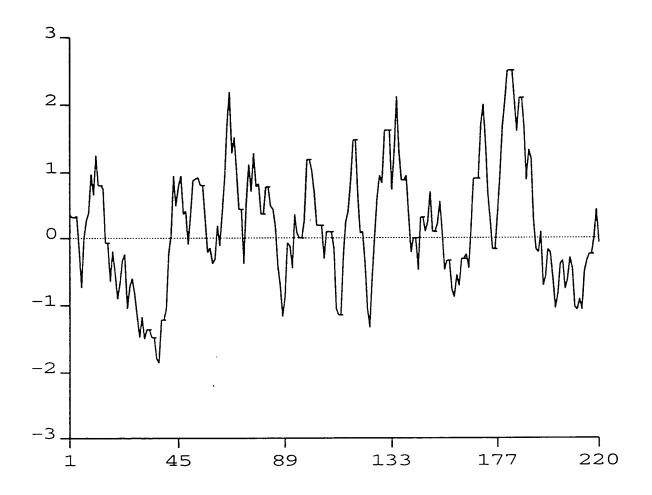
765 774 783 ACA TAG TGT TAC AAT ATT TAG AAA GTT TGA GC 3'

1 1 1	MAAEDVVATGADPSDLESGG MAAEDVVATGADPSELEGGG MAAEDVAATGADPSELEGGG	GI 1518818
21 21 21	LLHEIFTSPLNLLLLGLCIF LLQEIFTSPLNLLLLGLCIF LLHEIFTSPLNLLLLGLCIF	GI 1518818
41 41 41	LLYKIVRGDQPAASGD <u>RTTT</u> LLYKIVRGDQPGASGDNDDD LLYKIVRGDQPAAS-DSDDD	GI 1518818
61 61 60	X P P P L P R L K R R D F T P A E L R R E P P P L P R L K P R D F T P A E L R R E P P P L P R L K R R D F T P A E L R R	GI 1518818
81 81 80	FDGVQDPRILMAINGKVFDV YDGVQDPRILMAINGKVFDV FDGVQDPRILMAINGKVFDV	GI 1518818
101	T K G R K F Y G P E G P Y G V F A G R D T K G R K F Y G P E G P Y G V F A G R D T K G R K F Y G P E G P Y G V F A G R D	GI 1518818
121	ASRGLATFCLDKEALKDEYD ASRGLATFCLDKEALKDEYD ASRGLATFCLDKEALKDEYD	GI 1518818
141	DLSDLTAAQQETLSDWESQF DLSDLTPAQQETLNDWDSQF DLSDLTPAQQETLNDWDSQF	GI 1518818
161	TFKYHHV GKLLKEGEEPT SSPSSTITWGKLLEGAEEPI TFKYHHV GKLLKEGEEPT	GI 1518818

179 VYSDEEEPKDESSRKNVKAF 181 VYSDDEEQKMRLLGRVTEAV 178 VYSDEEEPKDESAR	
199 S G S I S X X Y F A K S F V T V H X V F	2504333
201 S G A Y L F L Y F A K S F V T F Q S V F	GI 1518818
192 K N D	GI 1657409
219 K T	2504333
221 T T W	GI 1518818
194	GI 1657409

Title: NOVEL HUMAN CYTOKINE/STEROID RECEPTOR PROTEIN

Serial No.: To Be Assigned



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